

#9

Patent Application US/07/599,543B

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## SEQUENCE LISTING

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## (1) GENERAL INFORMATION:

**Does not comply  
- Send a notice -**

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(i) APPLICANT: Opperman, Hermann  
Ozkaynak, Engin  
Rueger, David C.  
Kubera Sampath, Thangavel  
(ii) TITLE OF INVENTION: Osteogenic Proteins  
(iii) NUMBER OF SEQUENCES: 11  
(iv) CORRESPONDENCE ADDRESS:  
(A) ADDRESSEE: Testa Hurwitz & Thibeault  
(B) STREET: 53 State Street  
(C) CITY: Boston  
(D) STATE: Massachusetts  
(E) COUNTRY: U.S.A.  
(F) ZIP: 02109

21

(v) COMPUTER READABLE FORM:  
(A) MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage  
(B) COMPUTER: IBM XT  
(C) OPERATING SYSTEM: DOS 3.30  
(D) SOFTWARE: ASC II

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(vi) CURRENT APPLICATION DATA:  
(A) APPLICATION NUMBER: US 07/599,543  
(B) FILING DATE: 18-Oct-90

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(vii) PRIOR APPLICATION DATA: *insert*  
(A) APPLICATION NUMBER: US 569,920  
(B) FILING DATE: 20-Aug-90  
(C) APPLICATION NUMBER: US 315,342  
(D) FILING DATE: 23-Feb-89  
(E) APPLICATION NUMBER: US 422,699  
(F) FILING DATE: 17-Oct-89

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**(c) CLASSIFICATION:**

Patent Application US/07/599,543B

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71 (2) INFORMATION FOR SEQ ID NO:1:  
72 (i) SEQUENCE CHARACTERISTICS:  
73 (A) LENGTH: 139 amino acids  
74 (B) TYPE: amino acid  
75 (D) TOPOLOGY: linear  
76 (ii) MOLECULE TYPE: protein  
77 (ix) FEATURE:  
78 (A) NAME: mOP2 (mature)  
79 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:  
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81 Ala Ala Arg Pro Leu Lys Arg Arg Gln  
82 1 5  
83 Pro Lys Lys Thr Asn Glu Leu Pro His  
84 10 15  
85 Pro Asn Lys Leu Pro Gly Ile Phe Asp  
86 20 25  
87 Asp Gly His Gly Ser Arg Gly Arg Glu  
88 30 35  
89 Val Cys Arg Arg His Glu Leu Tyr Val  
90 40 45  
91 Arg Phe Arg Asp Leu Gly Trp Leu Asp  
92 50  
93 Trp Val Ile Ala Pro Gln Gly Tyr Ser  
94 55 60  
95 Ala Tyr Tyr Cys Glu Gly Glu Cys Ala  
96 65 70  
97 Phe Pro Leu Asp Ser Cys Met Asn Ala  
98 75 80  
99 Thr Asn His Ala Ile Leu Gln Ser Leu  
100 85 90  
101 Val His Leu Met Lys Pro Asp Val Val  
102 95  
103 Pro Lys Ala Cys Cys Ala Pro Thr Lys  
104 100 105  
105 Leu Ser Ala Thr Ser Val Leu Tyr Tyr  
106 110 115

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137 Asp Ser Ser Asn Asn Val Ile Leu Arg  
138 120 125  
139 Lys His Arg Asn Met Val Val Lys Ala  
140 130 135  
141 Cys Gly Cys His  
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144 (2) INFORMATION FOR SEQ ID NO:2:  
145 (i) SEQUENCE CHARACTERISTICS:  
146 (A) LENGTH: 1930 base pairs  
147 (B) TYPE: nucleic acid  
148 (C) STRANDEDNESS: single  
149 (D) TOPOLOGY: linear  
150 (ii) MOLECULE TYPE: cDNA  
151 (iii) HYPOTHETICAL: no  
152 (iv) ANTI-SENSE: no  
153 (vi) ORIGINAL SOURCE:  
154 (A) ORGANISM: mouse  
155 (F) TISSUE TYPE: embryo  
156 (ix) FEATURE:  
157 (A) NAME: mOP2  
158 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:  
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160 GGAATTCCGC TGCCAGGCAC AGGTGCGCCG TCTGGTCCTC 40  
161 CCCGTCTGGC GTCAGCCGAG CCCGACCAGC TACCAGTGGA 80  
162 TGC CGC GCCGG CTGAAAGTCC GAG ATG GCT ATG CGT 115  
163 Met Ala Met Arg  
164 1  
165 CCC GGG CCA CTC TGG CTA TTG GGC CTT GCT CTG 148  
166 Pro Gly Pro Leu Trp Leu Leu Gly Leu Ala Leu  
167 5 10 15  
168 TGC GCG CTG GGA GGC GGC CAC GGT CCC GGT CCC 181  
169 Cys Ala Leu Gly Gly His Gly Pro Gly Pro  
170 20 25  
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202 CCG CAC ACC TGT CCC CAG CGT CGC CTG GGA GCG 214  
203 Pro His Thr Cys Pro Gln Arg Arg Leu Gly Ala  
204 30 35  
205 CGC GAC CGG GAC ATG CAG CGT GAA ATC CTG CCG 247  
206 Arg Asp Arg Asp Met Gln Arg Glu Ile Leu Pro  
207 40 45  
208 GTG CTC GGG CTA CCG GGA CGC CCC GAC CCC GTG 280  
209 Val Leu Gly Leu Pro Gly Arg Pro Asp Pro Val  
210 50 55  
211 CAC AAC CCG CCG CTG CCC GGC ACG CAG CGT GCG 313  
212 His Asn Pro Pro Leu Pro Gly Thr Gln Arg Ala

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213 60 65 70  
214 CCC CTC TTC ATG TTG GAC CTA TAC CAC GCC ATG 346  
215 Pro Leu Phe Met Leu Asp Leu Tyr His Ala Met  
216 75 80  
217 ACC GAT GAC GAC GAC GGC GGG CCA CCA CAG GCT 379  
218 Thr Asp Asp Asp Asp Gly Gly Pro Pro Gln Ala  
219 85 90  
220 CAC TTA GGC CGT GCC GAC CTG GTC ATG AGC TTC 412  
221 His Leu Gly Arg Ala Asp Leu Val Met Ser Phe  
222 95 100  
223 GTC AAC ATG GTG GAA CGC GAC CGT ACC CTG GGC 445  
224 Val Asn Met Val Glu Arg Asp Arg Thr Leu Gly  
225 105 110  
226 TAC CAG GAG CCA CAC TGG AAG GAA TTC CAC TTT 478  
227 Tyr Gln Glu Pro His Trp Lys Glu Phe His Phe  
228 115 120 125  
229 GAC CTA ACC CAG ATC CCT GCT GGG GAG GCT GTC 511  
230 Asp Leu Thr Gln Ile Pro Ala Gly Glu Ala Val  
231 130 135  
232 ACA GCT GCT GAG TTC CGG ATC TAC AAA GAA CCC 544  
233 Thr Ala Ala Glu Phe Arg Ile Tyr Lys Glu Pro  
234 140 145  
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267 AGC ACC CAC CCG CTC AAC ACA ACC CTC CAC ATC 577  
268 Ser Thr His Pro Leu Asn Thr Thr Leu His Ile  
269 150 155  
270 AGC ATG TTC GAA GTG GTC CAA GAG CAC TCC AAC 610  
271 Ser Met Phe Glu Val Val Gln Glu His Ser Asn  
272 160 165  
273 AGG GAG TCT GAC TTG TTC TTT TTG GAT CTT CAG 643  
274 Arg Glu Ser Asp Leu Phe Leu Asp Leu Gln  
275 170 175 180  
276 ACG CTC CGA TCT GGG GAC GAG GGC TGG CTG GTG 676  
277 Thr Leu Arg Ser Gly Asp Glu Gly Trp Leu Val  
278 185 190  
279 CTG GAC ATC ACA GCA GCC AGT GAC CGA TGG CTG 709  
280 Leu Asp Ile Thr Ala Ala Ser Asp Arg Trp Leu  
281 195 200  
282 CTG AAC CAT CAC AAG GAC CTG GGA CTC CGC CTC 742  
283 Leu Asn His His Lys Asp Leu Gly Leu Arg Leu  
284 205 210  
285 TAT GTG GAA ACC GCG GAT GGG CAC AGC ATG GAT 775  
286 Tyr Val Glu Thr Ala Asp Gly His Ser Met Asp  
287 215 220  
288 CCT GGC CTG GCT GGT CTG CTT GGA CGA CAA GCA 808  
289 Pro Gly Leu Ala Gly Leu Leu Gly Arg Gln Ala  
290 225 230 235  
291 CCA CGC TCC AGA CAG CCT TTC ATG GTA ACC TTC 841  
292 Pro Arg Ser Arg Gln Pro Phe Met Val Thr Phe  
293 240 245  
294 TTC AGG GCC AGC CAG AGT CCT GTG CGG GCC CCT 874  
295 Phe Arg Ala Ser Gln Ser Pro Val Arg Ala Pro  
296 250 255  
297 CGG GCA GCG AGA CCA CTG AAG AGG AGG CAG CCA 907  
298 Arg Ala Ala Arg Pro Leu Lys Arg Arg Gln Pro  
299 260 265  
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332 AAG AAA ACG AAC GAG CTT CCG CAC CCC AAC AAA 940  
333 Lys Lys Thr Asn Glu Leu Pro His Pro Asn Lys  
334 270 275  
335 CTC CCA GGG ATC TTT GAT GAT GGC CAC GGT TCC 973  
336 Leu Pro Gly Ile Phe Asp Asp Gly His Gly Ser  
337 280 285 290  
338 CGC GGC AGA GAG GTT TGC CGC AGG CAT GAG CTC 1006  
339 Arg Gly Arg Glu Val Cys Arg Arg His Glu Leu  
340 295 300  
341 TAC GTC AGA TTC CGT GAC CTT GGC TGG CTG GAC 1039  
342 Tyr Val Arg Phe Arg Asp Leu Gly Trp Leu Asp  
343 305 310  
344 TGG GTC ATC GCC CCC CAG GGC TAC TCT GCC TAT 1072  
345 Trp Val Ile Ala Pro Gln Gly Tyr Ser Ala Tyr  
346 315 320  
347 TAC TGT GAG GGG GAG TGT GCT TTC CCA CTG GAC 1105  
348 Tyr Cys Glu Gly Glu Cys Ala Phe Pro Leu Asp  
349 325 330  
350 TCC TGT ATG AAC GCC ACC AAC CAT GCC ATC TTG 1138  
351 Ser Cys Met Asn Ala Thr Asn His Ala Ile Leu  
352 335 340 345  
353 CAG TCT CTG GTG CAC CTG ATG AAG CCA GAT GTT 1171  
354 Gln Ser Leu Val His Leu Met Lys Pro Asp Val  
355 350 355  
356 GTC CCC AAG GCA TGC TGT GCA CCC ACC AAA CTG 1204  
357 Val Pro Lys Ala Cys Cys Ala Pro Thr Lys Leu  
358 360 365  
359 AGT GCC ACC TCT GTG CTG TAC TAT GAC AGC AGC 1237  
360 Ser Ala Thr Ser Val Leu Tyr Tyr Asp Ser Ser  
361 370 375  
362 AAC AAT GTC ATC CTG CGT AAA CAC CGT AAC ATG 1270  
363 Asn Asn Val Ile Leu Arg Lys His Arg Asn Met  
364 380 385  
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397 GTG GTC AAG GCC TGT CGC TGC CAC 1294  
398 Val Val Lys Ala Cys Gly Cys His  
399 390 400  
400 TGAGGCCCG CCCAGCATCC TGCTTCTACT ACCTTACCAT 1334  
401 CTGGCCGGGC CCCTCTCCAG AGGCAGAAAC CCTTCTATGT 1374  
402 TATCATAGCT CAGACAGGGG CAATGGGAGG CCCTTCACTT 1414  
403 CCCCTGGCCA CTTCCCTGCTA AAATTCTGGT CTTTCCCAGT 1454  
404 TCCTCTGTCC TTCATGGGT TTCCGGGCTA TCACCCCGCC 1494  
405 CTCTCCATCC TCCTACCCCA AGCATAGACT GAATGCACAC 1534  
406 AGCATCCCAG AGCTATGCTA ACTGAGAGGT CTGGGGTCAG 1574  
407 CACTGAAGGC CCACATGAGG AAGACTGATC CTTGGCCATC 1614  
408 CTCAGCCCAC AATGGCAAAT TCTGGATGGT CTAAGAAGCC 1654  
409 CTGGAATTCT AAACTAGATG ATCTGGGCTC TCTGCACCAT 1694  
410 TCATTGTGGC AGTTGGGACA TTTTTAGGTA TAACAGACAC 1734  
411 ATACACTTAG ATCAATGCAT CGCTGTACTC CTTGAAATCA 1774  
412 GAGCTAGCTT GTTAGAAAAA GAATCAGAGC CAGGTATAGC 1814  
413 GGTGCATGTC ATTAATCCC GCGCTAAAGA GACAGAGACA 1854  
414 GGAGAATCTC TGTGAGTTCA AGGCCACATA GAAAGAGCCT 1894  
415 GTCTCGGGAG CAGGAAAAAA AAAAAAAACG GAATTCA 1930  
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418 (2) INFORMATION FOR SEQ ID NO:3:  
419 (i) SEQUENCE CHARACTERISTICS:  
420 (A) LENGTH: 139 amino acids  
421 (B) TYPE: amino acid  
422 (D) TOPOLOGY: linear  
423 (ii) MOLECULE TYPE: protein  
424 (ix) FEATURE:

## **Raw Sequence Listing**

07/08/91  
11:18:27

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425 (A) NAME: hOP2 (mature)  
 426 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3  
 427  
 428 Ala Val Arg Pro Leu Arg Arg Arg Gln  
 429 1 5  
 430 Pro Lys Lys Ser Asn Glu Leu Pro Gln  
 431 10 15  
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 464 Ala Asn Arg Leu Pro Gly Ile Phe Asp  
 465 20 25  
 466 Asp Val His Gly Ser His Gly Arg Gln  
 467 30 35  
 468 Val Cys Arg Arg His Glu Leu Tyr Val  
 469 40 45  
 470 Ser Phe Gln Asp Leu Gly Trp Leu Asp  
 471 50  
 472 Trp Val Ile Ala Pro Gln Gly Tyr Ser  
 473 55 60  
 474 Ala Tyr Tyr Cys Glu Gly Glu Cys Ser  
 475 65 70  
 476 Phe Pro Leu Asp Ser Cys Met Asn Ala  
 477 75 80

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478 Thr Asn His Ala Ile Leu Gln Ser Leu  
479 85 90  
480 Val His Leu Met Lys Pro Asn Ala Val  
481 95  
482 Pro Lys Ala Cys Cys Ala Pro Thr Lys  
483 100 105  
484 Leu Ser Ala Thr Ser Val Leu Tyr Tyr  
485 110 115  
486 Asp Ser Ser Asn Asn Val Ile Leu Arg  
487 120 125  
488 Lys Ala Arg Asn Met Val Val Lys Ala  
489 130 135  
490 Cys Gly Cys His  
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## 493 (2) INFORMATION FOR SEQ ID NO:4:

## 494 (i) SEQUENCE CHARACTERISTICS:

495 (A) LENGTH: 1956 base pairs

only 1941 are listed  
See line 797

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

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(D) TOPOLOGY: linear

530 (ii) MOLECULE TYPE: cDNA

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531 (iii) HYPOTHETICAL: no  
 532 (iv) ANTI-SENSE: no  
 533 (vi) ORIGINAL SOURCE:  
 534 (A) ORGANISM: homo sapiens  
 535 (F) TISSUE TYPE: hippocampus  
 536 (ix) FEATURE:  
 537 (A) NAME: hop2  
 538 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:  
 539  
 540 GGAATTCCGG CCACAGTGGC GCCGGCAGAG CAGGAGTGGC 40  
 541 TGGAGGAGCT GTGGTTGGAG CAGGAGGTGG CACGGCAGGG 80  
 542 CTGGAGGGCT CCCTATGAGT GGCGGAGACG GCCCAGGAGG 120  
 543 CGCTGGAGCA ACAGCTCCCACACCGCACCA AGCGGTGGCT 160  
 544 GCAGGAGCTC GCCCCATCGCC CCTGCGCTGC TCGGACCGCG 200  
 545 GCCACAGCCG GACTGGCGGG TACGGCGGGC ACAGAGGCAT 240  
 546 TGGCCGAGAG TCCCAGTCCG CAGAGTAGCC CCGGCCCTCGA 280  
 547 GGCGGTGGCG TCCCAGTCCT CTCCGTCCAG GAGCCAGGAC 320  
 548 AGGTGTGCGC CGGGCGGGCT CCAGGGACCG CGCCTGAGGC 360  
 549 CGGCTGCCCG CCCGTCCCACCG CCGCCCGCCCG CGCCCGCCCG 400  
 550 CCGCCGAGCC CAGCCTCCCTT GCCGTCGGGG CGTCCCCAGG 440  
 551 CCCTGGGTGGCG GCGCGGGAGC CGATGCGCGC CCGCTGAGCG 480  
 552 CCCCCAGCTGA GCGCCCCCGG CCTGCC ATG ACC GCG CTC 518  
 553 Met Thr Ala Leu  
 554 1  
 555 CCC GGC CCG CTC TGG CTC CTG GGC CTG GCG CTA 551  
 556 Pro Gly Pro Leu Trp Leu Leu Gly Leu Ala Leu  
 557 5 10 15  
 558 TGC GCG CTG GGC GGG GGC GGC CCC GGC CTG CGA 584  
 559 Cys Ala Leu Gly Gly Gly Pro Gly Leu Arg  
 560 20 25  
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594 CCC CCG CCC GGC TGT CCC CAG CGA CGT CTG GGC 617  
595 Pro Pro Pro Gly Cys Pro Gly arg Arg Leu Gly  
596 30 35  
597 GCG CGC GAC CGG GAC GTG CAG CGC GAG ATC CTG 650  
598 Ala Arg Asp Arg Asp Val Gln Arg Glu Ile Leu  
599 40 45  
600 GCG GTG CTC GGG CTG CCT GGG CGG CCC CGG CCC 683  
601 Ala Val Leu Gly Leu Pro Gly Arg Pro Arg Pro  
602 50 55  
603 CGC GCG CCA CCC GCC GCC TCC CGG CTG CCC GCG 716  
604 Arg Ala Pro Pro Ala Ala Ser Arg Leu Pro Ala  
605 60 65 70  
606 TCC GCG CCG CTC TTC ATG CTG GAC CTG TAC CAC 749  
607 Ser Ala Pro Leu Phe Met Leu Asp Leu Tyr His  
608 75 80  
609 CGC ATG GCC GGC GAC GAC GAC GAG GAC GGC GCC 782  
610 Arg Met Ala Gly Asp Asp Asp Glu Asp Gly Ala  
611 85 90  
612 GCG GAG GCC CTG GGC CGC GCC GAC CTG GTC ATG 815  
613 Ala Glu Ala Leu Gly Arg Ala Asp Leu Val Met  
614 95 100  
615 AGC TTC GTT AAC ATG GTG GAG CGA GAC CGT GCC 848  
616 Ser Phe Val Asn Met Val Glu Arg Asp Arg Ala  
617 105 110  
618 CTG GGC CAC CAG GAG CCC CAT TGG AAG GAG TTC 881  
619 Leu Gly His Gln Glu Pro His Trp Lys Glu Phe  
620 115 120 125  
621 CGC TTT GAC CTG ACC CAG ATC CCG GCT GGG GAG 914  
622 Arg Phe Asp Leu Thr Gln Ile Pro Ala Gly Glu  
623 130 135  
624 GCG GTC ACA GCT GCG GAG TTC CGG ATT TAC AAG 947  
625 Ala Val Thr Ala Ala Glu Phe Arg Ile Tyr Lys  
626 140 145  
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659 GTG CCC AGC ATC CAC CTG CTC AAC AGG ACC CTC 980  
660 Val Pro Ser Ile His Leu Leu Asn Arg Thr Leu  
661 150 155  
662 CAC GTC AGC ATG TTC CAG GTG GTC CAG GAG CAG 1013  
663 His Val Ser Met Phe Gln Val Val Gln Glu Gln  
664 160 165  
665 TCC AAC AGG GAG TCT GAC TTG TTC TTT TTG GAT 1046  
666 Ser Asn Arg Glu Ser Asp Leu Phe Phe Leu Asp  
667 170 175 180  
668 CTT CAG ACG CTC CGA GCT GGA GAC GAG GGC TGG 1079  
669 Leu Gln Thr Leu Arg Ala Gly Asp Glu Gly Trp  
670 185 190  
671 CTG GTG CTG GAT GTC ACA GCA GCC AGT GAC TGC 1112  
672 Leu Val Leu Asp Val Thr Ala Ala Ser Asp Cys  
673 195 200  
674 TGG TTG CTG AAG CGT CAC AAG GAC CTG GGA CTC 1145  
675 Trp Leu Leu Lys Arg His Lys Asp Leu Gly Leu  
676 205 210  
677 CGC CTC TAT GTG GAG ACT GAG GAC GGG CAC AGC 1178  
678 Arg Leu Tyr Val Glu Thr Glu Asp Gly His Ser  
679 215 220  
680 GTG GAT CCT GGC CTG GCC GGC CTG CTG GGT CAA 1211  
681 Val Asp Pro Gly Leu Ala Gly Leu Leu Gly Gln  
682 225 230 235  
683 CGG GCC CCA CGC TCC CAA CAG CCT TTC GTG GTC 1244  
684 Arg Ala Pro Arg Ser Gln Gln Pro Phe Val Val  
685 240 245  
686 ACT TTC TTC AGG GCC AGT CCG AGT CCC ATC CGC 1277  
687 Thr Phe Phe Arg Ala Ser Pro Ser Pro Ile Arg  
688 250 255  
689 ACC CCT CGG GCA GTG AGG CCA CTG AGG AGG AGG 1310

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690 Thr Pro Arg Ala Val Arg Pro Leu Arg Arg Arg  
691 260 265  
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724 CAG CCG AAG AAA AGC AAC GAG CTG CCG CAG GCC 1343  
725 Gln Pro Lys Lys Ser Asn Glu Leu Pro Gln Ala  
726 270 275  
727 AAC CGA CTC CCA GGG ATC TTT GAT GAC GTC CAC 1376  
728 Asn Arg Leu Pro Gly Ile Phe Asp Asp Val His  
729 280 285 290  
730 GGC TCC CAC GGC CGG CAG GTC TGC CGT CGG CAC 1409  
731 Gly Ser His Gly Arg Gln Val Cys Arg Arg His  
732 295 300  
733 GAG CTC TAC GTC AGC TTC CAG GAC CTC GGC TGG 1442  
734 Glu Leu Tyr Val Ser Phe Gln Asp Leu Gly Trp  
735 305 310  
736 CTG GAC TGG GTC ATC GCT CCC CAA GGC TAC TCG 1475  
737 Leu Asp Trp Val Ile Ala Pro Gln Gly Tyr Ser  
738 315 320  
739 GCC TAT TAC TGT GAG GGG GAG TGC TCC TTC CCA 1508  
740 Ala Tyr Tyr Cys Glu Gly Glu Cys Ser Phe Pro  
741 325 330  
742 CTG GAC TCC TGC ATG AAT GCC ACC AAC CAC GCC 1541

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743 Leu Asp Ser Cys Met Asn Ala Thr Asn His Ala  
744 335 340 345  
745 ATC CTG CAG TCC CTG GTG CAC CTG ATG AAG CCA 1574  
746 Ile Leu Gln Ser Leu Val His Leu Met Lys Pro  
747 350 355  
748 AAC GCA GTC CCC AAG GCG TGC TGT GCA CCC ACC 1607  
749 Asn Ala Val Pro Lys Ala Cys Cys Ala Pro Thr  
750 360 365  
751 AAG CTG AGC GCC ACC TCT GTG CTC TAC TAT GAC 1640  
752 Lys Leu Ser Ala Thr Ser Val Leu Tyr Tyr Asp  
753 370 375  
754 AGC AGC AAC AAC GTC ATC CTG CGC AAA GCC CGC 1673  
755 Ser Ser Asn Asn Val Ile Leu Arg Lys Ala Arg  
756 380 385  
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789 AAC ATG GTG GTC AAG GCC TGC GGC TGC CAC 1703  
790 Asn Met Val Val Lys Ala Cys Gly Cys His  
791 390 395  
792 TGAGTCAGCC CGCCCAGCCC TACTGCAGCA ATTCACTGGC 1743  
793 CGTCGTTTA CAACGTGTGA CTGGGAAAC CCTGGCGTTA 1783  
794 CCCAACTTAA TCGCCCTTGCA GCACATCCCC CTTTCGCCAG 1823  
795 CTGGCTAATA GCGAAGAGGC CCCGCACCGA TCGCCCTTCC 1863

796 CAACAGTTGC GCCCCAGTGA ATGGCGAATG GCAAATTGTA 1903  
797 AGCGTTAATA TTTTGTTAAA ATTTCGCGTTA AATTTTTT 1941 See line 495  
798  
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800 (2) INFORMATION FOR SEQ ID NO:5:  
801 (i) SEQUENCE CHARACTERISTICS:  
802 (A) LENGTH: 98 amino acids  
803 (B) TYPE: amino acid  
804 (D) TOPOLOGY: linear  
805 (ii) MOLECULE TYPE: protein  
806 (ix) FEATURE:  
807 (D) OTHER INFORMATION: wherein "res."

808 means "residue" and Xaa at res. 2 = (Lys or Arg); Xaa at  
809 res.3 = (Lys or Arg); Xaa res.9 = (Ser or Arg); Xaa at  
810 res.11 = (Arg or Gln); Xaa at res.16 = (Gln or Leu); Xaa  
811 at res. 19 = (Ile or Val); Xaa at res.23 = (Glu or Gln);  
812 Xaa at res.26 = (Ala or Ser); Xaa at res. 34 = (Ala or  
813 or Ser); Xaa at res.38= (Asn or Asp); Xaa at res. 40 =  
814 (Tyr or Cys); Xaa at res.49 = (Val or Leu); Xaa at  
815 res.52= (His or Asn); Xaa at res. 53 = (Phe or  
816 Leu); Xaa at res. 54 = (Ile or Met); Xaa at res. 55 = (Asn  
817 or Lys); Xaa at res. 56 = (Glu, Asp or Asn); Xaa at res.  
818 57=(Thr, Ala or Val); Xaa at res. 61 = (Pro or Ala);  
819 Xaa at res. 67=(gln or Lys); Xaa at res. 69 =  
820 (Asn or Ser); Xaa at 71=(Ile or Thr); Xaa at res.  
821 76= (Phe or Tyr); Xaa at res. 78 = (Asp, Glu or Ser);  
822 Xaa at res. 80= (Ser or Asn); Xaa at res. 84 = (Ile or  
823 Asp); Xaa at res. 85 Arg); Xaa at res. 87 = (Tyr, Ala  
824 or His); and Xaa at res. 93=(Arg or Lys)  
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826 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

828 Cys Xaa Xaa His Glu Leu Tyr Val Xaa Phe  
829 1 5 10  
830 Xaa Asp Leu Gly Trp Xaa Asp Trp Xaa Ile  
831 15 20  
832 Ala Pro Xaa Gly Tyr Xaa Ala Tyr Tyr Cys  
833 25 30  
834 Glu Gly Cys Xaa Phe Pro Leu Xaa Ser Xaa  
835 35 40  
836 Met Asn Ala Thr Asn His Ala Ile Xaa Thr  
837 45 50  
838 Leu Xaa Xaa Xaa Xaa Xaa Val  
839 55  
840 Pro Lys Xaa Cys Cys Ala Pro Thr Xaa Leu  
841 60 65

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874      Xaa    Ala Xaa    Ser Val Leu Tyr Xaa    Asp  
875                70    75  
876      Xaa    Ser Xaa    Asn Val Xaa    Leu Xaa    Lys  
877                80    85  
878      Xaa    Pro Asn Met Val Val Xaa    Ala Cys Gly  
879                90    95  
880      Cys His  
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882  
883 (2) INFORMATION FOR SEQ ID NO:6:  
884 (i) SEQUENCE CHARACTERISTICS:  
885        (A) LENGTH: 437 base pairs  
886        (B) TYPE: nucleic acid  
887        (C) STRANDEDNESS: single  
888        (D) TOPOLOGY: linear  
889 (ii) MOLECULE TYPE: cDNA  
890 (iii) HYPOTHETICAL: no  
891 (iv) ANTI-SENSE: no  
892 (vi) ORIGINAL SOURCE:  
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921 (A) ORGANISM: Human  
922 (F) TISSUE TYPE: placenta  
923 (ix) FEATURE:  
924 (A) NAME: OP1  
925 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

926  
927                           TCC ACG GGG         9  
928                           Ser Thr Gly  
929                           1  
930 AGC AAA CAG CGC AGC CAG AAC CGC TCC AAG ACG         42  
931 Ser Lys Gln Arg Ser Gln Asn Arg Ser Lys Thr  
932       5                  10  
933 CCC AAG AAC CAG GAA GCC CTG CGG ATG GCC AAC         75  
934 Pro Lys Asn Gln Glu Ala Leu Arg Met Ala Asn  
935       15                20                  25  
936 GTG GCA GAG AAC AGC AGC GAC CAG AGG CAG         108  
937 Val Ala Glu Asn Ser Ser Asp Gln Arg Gln  
938       30                35  
939 GCC TGT AAG AAG CAC GAG CTG TAT GTC AGC TTC         141  
940 Ala Cys Lys Lys His Glu Leu Tyr Val Ser Phe  
941       40                45  
942 CGA GAC CTG GGC TGG CAG GAC TGG ATC ATC GCG         174  
943 Arg Asp Leu Gly Trp Gln Asp Trp Ile Ile Ala  
944       50                55  
945 CCT GAA GGC TAC GCC GCC TAC TAC TGT GAG GGG         207  
946 Pro Glu Gly Tyr Ala Ala Tyr Tyr Cys Glu Gly  
947       60                65  
948 GAG TGT GCC TTC CCT CTG AAC TCC TAC ATG AAC         240  
949 Glu Cys Ala Phe Pro Leu Asn Ser Tyr Met Asn  
950       70                75                  80  
951 GCC ACC AAC CAC GCC ATC GTG CAG ACG CTG GTC         273  
952 Ala Thr Asn His Ala Ile Val Gln Thr Leu Val  
953       85                90  
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986 CAC TTC ATC AAC CCG GAA ACG GTG CCC AAG CCC 306  
987 His Phe Ile Asn Pro Glu Thr Val Pro Lys Pro  
988 95 100  
989 TGC TGT GCG CCC ACG CAG CTC AAT GCC ATC TCC 339  
990 Cys Cys Ala Pro Thr Gln Leu Asn Ala Ile Ser  
991 105 110  
992 GTC CTC TAC TTC GAT GAC AGC TCC AAC GTC ATC 372  
993 Val Leu Tyr Phe Asp Asp Ser Ser Asn Val Ile  
994 115 120  
995 CTG AAG AAA TAC AGA AAC ATG GTG GTC CGG GCC 405  
996 Leu Lys Lys Tyr Arg Asn Met Val Val Arg Ala  
997 125 130 135  
998 TGT GGC TGC CAC TAGCTCCTCC GAGAATTCAG 437  
999 Cys Gly Cys His  
1000  
1001  
1002 (2) INFORMATION FOR SEQ ID NO:7:  
1003 (i) SEQUENCE CHARACTERISTICS:  
1004 (A) LENGTH: 102 amino acids  
1005 (B) TYPE: amino acid  
1006 (D) TOPOLOGY: linear  
1007 (ii) MOLECULE TYPE: protein

## Patent Application US/07/599,543B

1008 (ix) FEATURE:

1009 (D) OTHER INFORMATION:

1010 wherein each Xaa independently represents one of  
1011 the 20 naturally occurring L-isomer, α-amino acids.

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1013 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

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1015 Cys Xaa  
1016 1 5 101017 Xaa  
1018 15 201019 Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa  
1020 25 301021 Cys Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa  
1022 35 401023 Xaa  
1024 45 50 55

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1056 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys  
1057 60 651058 Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
1059 70 75

1060 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa

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1061               80               85  
1062 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys  
1063               90               95  
1064 Xaa Cys Xaa  
1065               100  
1066

## 1067 (2) INFORMATION FOR SEQ ID NO:8:

1068 (i) SEQUENCE CHARACTERISTICS:  
1069       (A) LENGTH: 97 amino acids  
1070       (B) TYPE: amino acid  
1071       (D) TOPOLOGY: linear  
1072 (ii) MOLECULE TYPE: protein  
1073 (ix) FEATURE:  
1074       (D) OTHER INFORMATION:

1075 wherein each Xaa independently represents one of  
1076 the 20 naturally occurring L-isomer, a-amino acids

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1078 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

1080 Xaa  
1081       1               5               10  
1082 Xaa  
1083       15              20  
1084 Xaa Xaa Cys Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa  
1085       25              30  
1086 Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
1087       35              40  
1088 Xaa  
1089       45              50              55

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## Patent Application US/07/599,543B

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1122 Xaa Xaa Xaa Xaa Xaa Cys Cys Xaa Xaa Xaa Xaa  
1123 60 65  
1124 Xaa  
1125 70 75  
1126 Xaa  
1127 80 85  
1128 Xaa Xaa Xaa Xaa Cys Xaa Cys Xaa  
1129 90 95  
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1132 (2) INFORMATION FOR SEQ ID NO:9:  
1133 (i) SEQUENCE CHARACTERISTICS:  
1134 (A) LENGTH: 136 amino acids  
1135 (B) TYPE: amino acid  
1136 (D) TOPOLOGY: linear  
1137 (ii) MOLECULE TYPE: protein  
1138 (ix) FEATURE:  
1139 (A) NAME: hOP-2P  
1140 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:  
1141  
1142 Pro Leu Arg Arg Arg Gln  
1143 1 5  
1144 Pro Lys Lys Ser Asn Glu Leu Pro Gln  
1145 10 15  
1146 Ala Asn Arg Leu Pro Gly Ile Phe Asp  
1147 20  
1148 Asp Val Asn Gly Ser His Gly Arg Gln  
1149 25 30  
1150 Val Cys Arg Arg His Glu Leu Tyr Val  
1151 35 40  
1152 Ser Phe Gln Asp Leu Gly Trp Leu Asp  
1153 45 50  
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1220 Pro Lys Lys Ser Asn Glu Leu Pro Gln  
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1253 Ala Asn Arg Leu Pro Gly Ile Phe Asp  
1254 15 20

1255 Asp Val Asn Gly Ser His Gly Arg Gln  
1256 25 30

1257 Val Cys Arg Arg His Glu Leu Tyr Val  
1258 35

1259 Ser Phe Gln Asp Leu Gly Trp Leu Asp  
1260 40 45

1261 Tyr Val Ile Ala Pro Gln Gly Tyr Ser  
1262 50 55

1263 Ala Tyr Tyr Cys Glu Gly Glu Cys Ser  
1264 60 65

1265 Phe Pro Leu Asp Ser Cys Met Asn Ala  
1266 70 75

1267 Thr Asn His Ala Ile Leu Gln Ser Leu  
1268 80

1269 Val His Leu Met Lys Pro Asn Ala Val  
1270 85 90

1271 Pro Lys Ala Cys Cys Ala Pro Thr Lys  
1272 95 100

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1186 Tyr Val Ile Ala Pro Gln Gly Tyr Ser  
1187 55 60  
1188 Ala Tyr Tyr Cys Glu Gly Glu Cys Ser  
1189 65  
1190 Phe Pro Leu Asp Ser Cys Met Asn Ala  
1191 70 75  
1192 Thr Asn His Ala Ile Leu Gln Ser Leu  
1193 80 85  
1194 Val His Leu Met Lys Pro Asn Ala Val  
1195 90 95  
1196 Pro Lys Ala Cys Cys Ala Pro Thr Lys  
1197 100 105  
1198 Leu Ser Ala Thr Ser Val Leu Tyr Tyr  
1199 110  
1200 Asp Glu Ser Asn Asn Val Ile Leu Arg  
1201 115 120  
1202 Lys Ala Arg Asn Met Val Val Lys Ala  
1203 125 130  
1204 Cys Gly Cys His. *(C) not valid, please delete*  
1205 135  
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1208 (2) INFORMATION FOR SEQ ID NO:10:  
1209 (i) SEQUENCE CHARACTERISTICS:  
1210 (A) LENGTH: 133 amino acids  
1211 (B) TYPE: amino acid  
1212 (D) TOPOLOGY: linear  
1213 (ii) MOLECULE TYPE: protein  
1214 (ix) FEATURE:  
1215 (A) NAME: hOP-2R  
1216 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:  
1217  
1218 Arg Arg Gln  
1219 1

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1273 Leu Ser Ala Thr Ser Val Leu Tyr Tyr  
1274 105 110  
1275 Asp Glu Ser Asn Asn Val Ile Leu Arg  
1276 115 120  
1277 Lys Ala Arg Asn Met Val Val Lys Ala  
1278 125  
1279 Cys Gly Cys His ~~His~~ *delete*  
1280 130

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1283 (2) INFORMATION FOR SEQ ID NO:11:

1284 (i) SEQUENCE CHARACTERISTICS:

1285 (A) LENGTH: 170 amino acids 160  
1286 (B) TYPE: amino acid

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1317 (D) TOPOLOGY: linear

1318 (ii) MOLECULE TYPE: protein

1319 (ix) FEATURE:

1320 (A) NAME: hOP-2S

1321 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

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1323 Ser Gln Gln

1324 1

1325 Pro Phe Val Val Thr Phe Phe Arg Ala



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1384 Leu Ser Ala Thr Ser Val Leu Tyr Tyr  
1385 130 135  
1386 Asp Glu Ser Asn Asn Val Ile Leu Arg  
1387 140 145  
1388 Lys Ala Arg Asn Met Val Val Lys Ala  
1389 150 165  
1390 Cys Gly Cys His 155  
1391 170  
1392 160  
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Page: 28

**Raw Sequence Listing**

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**Patent Application US/07/599,543B**

1432  
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## LINE ERROR

## ORIGINAL TEXT

27 Wrong application Serial Number  
538 Entered and Calc. Seq. Length differ  
811 Response Exceeds Line Limitations  
812 Response Exceeds Line Limitations  
813 Response Exceeds Line Limitations  
814 Response Exceeds Line Limitations  
815 Response Exceeds Line Limitations  
816 Response Exceeds Line Limitations  
817 Response Exceeds Line Limitations  
818 Response Exceeds Line Limitations  
819 Response Exceeds Line Limitations  
820 Response Exceeds Line Limitations  
821 Response Exceeds Line Limitations  
822 Response Exceeds Line Limitations  
823 Response Exceeds Line Limitations  
824 Response Exceeds Line Limitations  
1204 Wrong Amino Acid Designator  
1140 Entered and Calc. Seq. Length differ  
1279 Wrong Amino Acid Designator  
1216 Entered and Calc. Seq. Length differ  
1321 Entered and Calc. Seq. Length differ

OK →(A) APPLICATION NUMBER: US 07/599,543  
see p.15 →(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:  
at res. 19 = (Ile or Val); Xaa at res. 23  
Xaa at res. 26 = (Ala or Ser); Xaa at res.  
or Ser); Xaa at res. 38= (Asn or Asp); Xa  
(Tyr or Cys); Xaa at res. 49 = (Val or Le  
res.52= (His or Asn); Xaa at res. 53 = (Leu);  
Xaa at res. 54 = (Ile or Met); Xaa  
or Lys); Xaa at res. 56 = (Glu, Asp or A  
57=(Thr, Ala or Val); Xaa at res. 61 = (Xaa  
at res. 67=(gln or Lys); Xaa at res.  
(Asn or Ser); Xaa at 71=(Ile or Thr); Xa  
76= (Phe or Tyr); Xaa at res. 78 = (Asp,  
Xaa at res. 80= (Ser or Asn); Xaa at res.  
Asp); Xaa at res. 85 Arg); Xaa at res. 8  
or His); and Xaa at res. 93=(Arg or Lys)  
Cys Gly Cys His ~~O~~ delete  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:  
Cys Gly Cys His ~~O~~  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

4 line limit, but o.k. here

PAGE: 1

SEQUENCE MISSING ITEM REPORT  
PATENT APPLICATION US/07/599,543B

DATE: 07/08/91  
TIME: 11:20:48

MANDATORY IDENTIFIER THAT WAS NOT FOUND

CLASSIFICATION

PAGE: 1

SEQUENCE CORRECTION REPORT  
PATENT APPLICATION US/07/599,543B

DATE: 07/08/91  
TIME: 11:20:48

LINE ORIGINAL TEXT

78 (A) NAME: mOP2 (mature)  
157 (A) NAME: mOP2  
425 (A) NAME: hOP2 (mature)  
537 (A) NAME: hOP2  
924 (A) NAME: OP1  
1139 (A) NAME: hOP-2P  
1215 (A) NAME: hOP-2R  
1320 (A) NAME: hOP-2S

CORRECTED TEXT

(A) NAME/KEY: mOP2 (mature)  
(A) NAME/KEY: mOP2  
(A) NAME/KEY: hOP2 (mature)  
(A) NAME/KEY: hOP2  
(A) NAME/KEY: OP1  
(A) NAME/KEY: hOP-2P  
(A) NAME/KEY: hOP-2R  
(A) NAME/KEY: hOP-2S